



1600

RAW SEQUENCE LISTING

DATE: 01/15/2004

PATENT APPLICATION: US/09/762,767B

TIME: 10:02:00

Input Set : A:\VOS-101SEQLIST.TXT

Output Set: N:\CRF4\01152004\I762767B.raw

4 <110> APPLICANT: SCHMIDT, Harald
 5 ZABEL, Ulrike
 6 POLLER, Wolfgang
 8 <120> TITLE OF INVENTION: Isolated and Purified Human Soluble
 9 Guanylylcyclase alphas/betas (hsGC alphas/betas)
 12 <130> FILE REFERENCE: VOS-101
 14 <140> CURRENT APPLICATION NUMBER: US 09/762,767B
 15 <141> CURRENT FILING DATE: 2001-06-01
 17 <150> PRIOR APPLICATION NUMBER: PCT/DE99/02601
 18 <151> PRIOR FILING DATE: 1999-08-16
 20 <150> PRIOR APPLICATION NUMBER: DE 198 37 015.6
 21 <151> PRIOR FILING DATE: 1998-08-14
 23 <160> NUMBER OF SEQ ID NOS: 19
 25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 3015
 29 <212> TYPE: DNA
 30 <213> ORGANISM: homo sapiens
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 35 ttcttacact ttctctgcgc tagagcagcg agcagcctgg aacagacca ggcggaggag 180
 36 acctgtgggg gaggagcgc ctggaggagc tttagagacc cagccgggcg tgatctcacc 240
 37 atgtgcggaat ttgcgagcg cgccctggag ctgctagaga tccggaagca cagccccgag 300
 38 gtgtgcgaag ccaccaagac tgcggtcttt ggagaaagcg tgagcagggg gccaccgcgg 360
 39 tctccgcgcc tgtctgcacc ctgtgccttg agctgcctga cagtgcacat gacatcccag 420
 40 ttaccagtgt ccttgaattg atagtggctt ctgtttgtca gtctcatata agaactacag 480
 41 ctcatcagga ggagatcgca gcagggtaag agacaccaac accatgttct gcacgaagct 540
 42 caaggatctc aagatcacag gagagtgtcc tttctcctta ctggcaccag gtcaagttcc 600
 43 taacgagtct tcagaggagg cagcaggaag cttagagagc tgcaaagcaa ccgtgcccac 660
 44 ctgtcaagac attcctgaga agaacatata agaaagtctt cctcaaaga aaaccagtcg 720
 45 gagccgagtc tatcttcaca ctttggcaga gagtatttgc aaactgattt tcccagagtt 780
 46 tgaacggctg aatgttgac ttcagagaac attggcaaag caaaaataa aagaaagcag 840
 47 gaaatctttg gaaagagaag actttgaaaa acaattgca gagcaagcag ttgcagcagg 900
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57 aaggctgatg aacaggagag actttcaagg aaagcctaata tttgaagaat actttgaaat 1500
58 tctgactcca aaaatcaacc agacgttttag cgggatcatg actatgttga atatgcagtt 1560
59 tgttgtacga gtgaggagat gggacaactc tgtgaagaaa tcttcaagggt ttatggacct 1620
60 caaaggccaa atgatctaca ttgttgaatc cagtgcatac ttgtttttgg ggtcaccctg 1680
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62 caatgcactg agggatgtgg tcttaatagg ggaacaagcc cgagctcaag atggcctgaa 1800
63 gaagaggctg ggggaagctga aggctaccct tgagcaagcc caccaagccc tggaggagga 1860
64 gaagaaaaag acagtagacc ttctgtgctc catattttccc tgtgaggttg ctccagcagct 1920
65 gtggcaagggt caagtgtgtc aagccaagaa gttcagtaat gtcaccatgc tcttctcaga 1980
66 catcgttggg ttcactgcca tctgctccca gtgctcaccg ctgcagggtca tcaccatgct 2040
67 caatgcactg tacactcgct tcgaccagca gtgtggagag ctggatgtct acaagggtga 2100
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70 ccattggagaa cctatcaaga tgcgaattgg actgcactct ggatcagttt ttgctggcgt 2280
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85 <210> SEQ ID NO: 2

86 <211> LENGTH: 688

87 <212> TYPE: PRT

88 <213> ORGANISM: homo sapiens

90 <400> SEQUENCE: 2

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93 Phe Ser Leu Leu Ala Pro Gly Gln Val Pro Asn Glu Ser Ser Glu Glu
94 20 25 30
95 Ala Ala Gly Ser Ser Glu Ser Cys Lys Ala Thr Val Pro Ile Cys Gln
96 35 40 45
97 Asp Ile Pro Glu Lys Asn Ile Gln Glu Ser Leu Pro Gln Arg Lys Thr
98 50 55 60
99 Ser Arg Ser Arg Val Tyr Leu His Thr Leu Ala Glu Ser Ile Cys Lys
100 65 70 75 80
101 Leu Ile Phe Pro Glu Phe Glu Arg Leu Asn Val Ala Leu Gln Arg Thr
102 85 90 95
103 Leu Ala Lys His Lys Ile Lys Glu Ser Arg Lys Ser Leu Glu Arg Glu
104 100 105 110
105 Asp Phe Glu Lys Thr Ile Ala Glu Gln Ala Val Ala Ala Gly Val Pro
106 115 120 125
107 Val Glu Val Ile Lys Glu Ser Leu Gly Glu Glu Val Phe Lys Ile Cys

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108      130      135      140
109 Tyr Glu Glu Asp Glu Asn Ile Leu Gly Val Val Gly Gly Thr Leu Lys
110 145      150      155      160
111 Asp Phe Leu Asn Ser Phe Ser Thr Leu Leu Lys Gln Ser Ser His Cys
112      165      170      175
113 Gln Glu Ala Gly Lys Arg Gly Arg Leu Glu Asp Ala Ser Ile Leu Cys
114      180      185      190
115 Leu Asp Lys Glu Asp Asp Phe Leu His Val Tyr Tyr Phe Phe Pro Lys
116      195      200      205
117 Arg Thr Thr Ser Leu Ile Leu Pro Gly Ile Ile Lys Ala Ala Ala His
118      210      215      220
119 Val Leu Tyr Glu Thr Glu Val Glu Val Ser Leu Met Pro Pro Cys Phe
120 225      230      235      240
121 His Asn Asp Cys Ser Glu Phe Val Asn Gln Pro Tyr Leu Leu Tyr Ser
122      245      250      255
123 Val His Met Lys Ser Thr Lys Pro Ser Leu Ser Pro Ser Lys Pro Gln
124      260      265      270
125 Ser Ser Leu Val Ile Pro Thr Ser Leu Phe Cys Lys Thr Phe Pro Phe
126      275      280      285
127 His Phe Met Phe Asp Lys Asp Met Thr Ile Leu Gln Phe Gly Asn Gly
128      290      295      300
129 Ile Arg Arg Leu Met Asn Arg Arg Asp Phe Gln Gly Lys Pro Asn Phe
130 305      310      315      320
131 Glu Glu Tyr Phe Glu Ile Leu Thr Pro Lys Ile Asn Gln Thr Phe Ser
132      325      330      335
133 Gly Ile Met Thr Met Leu Asn Met Gln Phe Val Val Arg Val Arg Arg
134      340      345      350
135 Trp Asp Asn Ser Val Lys Lys Ser Ser Arg Val Met Asp Leu Lys Gly
136      355      360      365
137 Gln Met Ile Tyr Ile Val Glu Ser Ser Ala Ile Leu Phe Leu Gly Ser
138      370      375      380
139 Pro Cys Val Asp Arg Leu Glu Asp Phe Thr Gly Arg Gly Leu Tyr Leu
140 385      390      395      400
141 Ser Asp Ile Pro Ile His Asn Ala Leu Arg Asp Val Val Leu Ile Gly
142      405      410      415
143 Glu Gln Ala Arg Ala Gln Asp Gly Leu Lys Lys Arg Leu Gly Lys Leu
144      420      425      430
145 Lys Ala Thr Leu Glu Gln Ala His Gln Ala Leu Glu Glu Glu Lys Lys
146      435      440      445
147 Lys Thr Val Asp Leu Leu Cys Ser Ile Phe Pro Cys Glu Val Ala Gln
148      450      455      460
149 Gln Leu Trp Gln Gly Gln Val Val Gln Ala Lys Lys Phe Ser Asn Val
150 465      470      475      480
151 Thr Met Leu Phe Ser Asp Ile Val Gly Phe Thr Ala Ile Cys Ser Gln
152      485      490      495
153 Cys Ser Pro Leu Gln Val Ile Thr Met Leu Asn Ala Leu Tyr Thr Arg
154      500      505      510
155 Phe Asp Gln Gln Cys Gly Glu Leu Asp Val Tyr Lys Val Glu Thr Ile
156      515      520      525

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157 Gly Asp Ala Tyr Cys Val Ala Gly Gly Leu His Lys Glu Ser Asp Thr
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159 His Ala Val Gln Ile Ala Leu Met Ala Leu Lys Met Met Glu Leu Ser
160 545      550      555      560
161 Asp Glu Val Met Ser Pro His Gly Glu Pro Ile Lys Met Arg Ile Gly
162      565      570      575
163 Leu His Ser Gly Ser Val Phe Ala Gly Val Val Gly Val Lys Met Pro
164      580      585      590
165 Arg Tyr Cys Leu Phe Gly Asn Asn Val Thr Leu Ala Asn Lys Phe Glu
166      595      600      605
167 Ser Cys Ser Val Pro Arg Lys Ile Asn Val Ser Pro Thr Thr Tyr Arg
168      610      615      620
169 Leu Leu Lys Asp Cys Pro Gly Phe Val Phe Thr Pro Arg Ser Arg Glu
170 625      630      635      640
171 Glu Leu Pro Pro Asn Phe Pro Ser Glu Ile Pro Gly Ile Cys His Phe
172      645      650      655
173 Leu Asp Ala Tyr Gln Gln Gly Thr Asn Ser Lys Pro Cys Phe Gln Lys
174      660      665      670
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179 <210> SEQ ID NO: 3
180 <211> LENGTH: 2443
181 <212> TYPE: DNA
182 <213> ORGANISM: homo sapiens
184 <400> SEQUENCE: 3
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187 gctggtgatc cgcaattacg gccccgaggt gtgggaagac atcaaaaaag aggcacagtt 180
188 agatgaagaa ggacagtttc ttgtcagaat aatatatgat gactccaaaaa cttatgattt 240
189 ggttgctgct gcaagcaaaag tcctcaatct caatgctgga gaaatcctcc aaatgttttg 300
190 gaagatgttt ttcgtctttt gccagaatc tggttatgat acaatcttgc gtgtcctggg 360
191 ctctaattgc agagaatttc tacagaacct tgatgctctg cacgaccacc ttgctaccat 420
192 ctaccagga atgcgtgcac ctctctttag gtgcaactgt gcagaaaagg gcaaaggact 480
193 cattttgcac tactactcag agagagaagg acttcaggat attgtcattg gaatcatcaa 540
194 aacagtggca caacaaatcc atggcactga aatagacatg aaggttattc agcaaagaaa 600
195 tgaagaatgt gatcatactc aatttttaat tgaagaaaaa gagtcaaaag aagaggattt 660
196 ttatgaagat cttgacagat ttgaagaaaa tggtagccag gaatcacgca tcagcccata 720
197 tacattctgc aaagcttttc cttttcatat aatatttgac cgggacctag tggtagctca 780
198 gtgtggcaat gctatataca gagttctccc ccagctccag cctgggaatt gcagccttct 840
199 gtctgtcttc tcgctggttc gtcctcatat tgatattagt ttccatggga tcctttctca 900
200 atcaataact gtttttgtat tgagaagcaa ggaaggattg ttggatgtgg agaaattaga 960
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203 cgatttgaca aggagagggc tgtatctaag tgcacccct ctgcatgatg ccacgcgcga 1140
204 tcttgttctt ttgggagaac aatttagaga ggaatacaaa ctcaccaag aactggaaat 1200
205 cctcactgac aggctacagc tcacgttaag agccctggaa gatgaaaaga aaaagacaga 1260
206 cacattgctg tattctgtcc ttctccgtc tgttgccaat gagctgcggc acaagcgtcc 1320
207 agtgctgcc aaaagatatg acaatgtgac catcctcttt agtggcattg tgggcttcaa 1380
208 tgctttctgt agcaagcatg catctggaga aggagccatg aagatcgtca acctcctcaa 1440

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209 cgacctctac accagatttg acacactgac tgattcccgg aaaaacccat ttgtttataa 1500
210 ggtggagact gttggtgaca agtatatgac agtgagtggg ttaccagagc catgcattca 1560
211 ccatgcacga tccatctgcc acctggcctt ggacatgatg gaaattgctg gccaggttca 1620
212 agtagatggt gaatctgttc agataacaat agggatacac actggagagg tagttacagg 1680
213 tgtcatagga cagcggatgc ctcgatactg tctttttggg aatactgtca acctcacaag 1740
214 ccgaacagaa accacaggag aaaagggaaa aataaatgtg tctgaatata catacagatg 1800
215 tcttatgtct ccagaaaatt cagatccaca attccacttg gagcacagag gcccagtgtc 1860
216 catgaagggc aaaaaagaac caatgcaagt ttggtttcta tccagaaaaa atacaggaac 1920
217 agaggaaaca aagcaggatg atgactgaat cttggattat ggggtgaaga ggagtacaga 1980
218 ctaggttcca gttttctcct aacacgtgcc aagcccagga gcagttcttc cctatggata 2040
219 cagatattct tttgtccttg tccattaccc caagactttc ttctagatat atctctcact 2100
220 atccggtatt caaccttagc tctgctttct attacttttt aggccttagt atattatcta 2160
221 aagttttgct tttgatgtgg atgatgtgag cttcatgtgt cttaaaatct actacaagca 2220
222 ttaccttaaca tggatgctg caagtagtag gcaccaata aatatttggt gaatttagtt 2280
223 aaatgaaact gaacagtgtt tggccatgtg tatatttata tcatgtttac caaatctggt 2340
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227 <210> SEQ ID NO: 4

228 <211> LENGTH: 619

229 <212> TYPE: PRT

230 <213> ORGANISM: homo sapiens

232 <400> SEQUENCE: 4

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236 20 25 30
237 Glu Glu Gly Gln Phe Leu Val Arg Ile Ile Tyr Asp Asp Ser Lys Thr
238 35 40 45
239 Tyr Asp Leu Val Ala Ala Ala Ser Lys Val Leu Asn Leu Asn Ala Gly
240 50 55 60
241 Glu Ile Leu Gln Met Phe Gly Lys Met Phe Phe Val Phe Cys Gln Glu
242 65 70 75 80
243 Ser Gly Tyr Asp Thr Ile Leu Arg Val Leu Gly Ser Asn Val Arg Glu
244 85 90 95
245 Phe Leu Gln Asn Leu Asp Ala Leu His Asp His Leu Ala Thr Ile Tyr
246 100 105 110
247 Pro Gly Met Arg Ala Pro Ser Phe Arg Cys Thr Asp Ala Glu Lys Gly
248 115 120 125
249 Lys Gly Leu Ile Leu His Tyr Tyr Ser Glu Arg Glu Gly Leu Gln Asp
250 130 135 140
251 Ile Val Ile Gly Ile Ile Lys Thr Val Ala Gln Gln Ile His Gly Thr
252 145 150 155 160
253 Glu Ile Asp Met Lys Val Ile Gln Gln Arg Asn Glu Glu Cys Asp His
254 165 170 175
255 Thr Gln Phe Leu Ile Glu Glu Lys Glu Ser Lys Glu Glu Asp Phe Tyr
256 180 185 190
257 Glu Asp Leu Asp Arg Phe Glu Glu Asn Gly Thr Gln Glu Ser Arg Ile
258 195 200 205
259 Ser Pro Tyr Thr Phe Cys Lys Ala Phe Pro Phe His Ile Ile Phe Asp

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